

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1841	100.0	1841	6	AX253204	AX253204 Sequence
2	1841	100.0	1841	6	AX365258	AX365258 Sequence
3	1805	98.0	1818	6	AX191534	AX191534 Sequence
4	1800.2	97.8	2171	6	AR448094	AR448094 Sequence
5	1794.6	97.5	2042	9	BC000980	BC000980 Homo sapi
6	1790.2	97.2	1796	6	AX350967	AX350967 Sequence
7	1786	97.0	1828	9	AF208110	AF208110 Homo sapi
8	1776.6	96.5	1918	6	AR256118	AR256118 Sequence
9	1769.8	96.1	1816	9	AF212365	AF212365 Homo sapi
10	1769.4	96.1	1816	6	AR256107	AR256107 Sequence
11	1769.4	96.1	1816	6	AR410121	AR410121 Sequence
12	1607.4	87.3	2015	6	AX253207	AX253207 Sequence
13	1607.4	87.3	2015	6	AX365260	AX365260 Sequence
14	1573.4	85.5	1713	6	AX253209	AX253209 Sequence
15	1558.2	84.6	1583	9	AF250309	AF250309 Homo sapi
16	1539	83.6	1701	6	AR306577	AR306577 Sequence
17	1539	83.6	1701	6	AX061651	AX061651 Sequence
18	1513.4	82.2	1515	6	AR338361	AR338361 Sequence
19	1513.4	82.2	1515	6	AX092426	AX092426 Sequence
20	1513.4	82.2	1515	6	AX180774	AX180774 Sequence
21	1513.4	82.2	1515	6	AX376332	AX376332 Sequence
22	1513.4	82.2	1515	9	AY359122	AY359122 Homo sapi
23	1505.8	81.8	1509	6	AX191524	AX191524 Sequence
24	1504.2	81.7	1509	12	BT007692	BT007692 Synthetic
25	1191.8	64.7	1362	6	CQ716823	CQ716823 Sequence
26	1082.8	58.8	1506	6	AX350969	AX350969 Sequence
27	1040.2	56.5	2856	9	AF208111	AF208111 Homo sapi
28	988.2	53.7	1963	10	AF208108	AF208108 Mus muscu
29	980.8	53.3	2018	10	BC026546	BC026546 Mus muscu
30	940.2	51.1	2080	6	BD275570	BD275570 MOLECULES
c 31	842.2	45.7	7164	6	BD185215	BD185215 Novel gen
32	842.2	45.7	22531	9	AY518533	AY518533 Homo sapi

c	33	842.2	45.7	149634	9	AC113172	AC113172 Homo sapi
c	34	842.2	45.7	177072	9	AC012467	AC012467 Homo sapi
	35	643.2	34.9	2589	10	AF208109	AF208109 Mus muscu
	36	378.2	20.5	234131	2	AC093357	AC093357 Mus muscu
c	37	359.4	19.5	234122	2	AC137172	AC137172 Rattus no
c	38	359.4	19.5	251412	2	AC136586	AC136586 Rattus no
	39	328	17.8	409	6	AR256108	AR256108 Sequence
	40	328	17.8	409	6	AR410122	AR410122 Sequence
c	41	263.6	14.3	507	11	G29993	G29993 human STS S
	42	244	13.3	374	6	AX098181	AX098181 Sequence
c	43	200.6	10.9	201	11	BV175040	BV175040 sqnm76293
	44	187.2	10.2	327	6	AR256109	AR256109 Sequence
	45	187.2	10.2	327	6	AR410123	AR410123 Sequence

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1841	100.0	1841	6	AAD28776	Aad28776 Human Int
2	1841	100.0	1841	6	ABA03200	Aba03200 Human IL-
3	1841	100.0	1841	12	ADE83326	Ade83326 Human IL-
4	1805	98.0	1818	4	AAD12581	Aad12581 Human pro
5	1800.2	97.8	2171	12	ADL13033	Adl13033 Human ste
6	1790.6	97.3	2161	4	AAH99008	Aah99008 Human EST
7	1790.2	97.2	1796	6	AAS18126	Aas18126 Human DNA
8	1786	97.0	1827	4	AAD13443	Aad13443 Human int
9	1776.6	96.5	1918	3	AAZ52046	Aaz52046 cDNA enco
10	1776.6	96.5	1918	3	AAA75772	Aaa75772 cDNA enco
11	1769.8	96.1	1816	12	ADI37001	Adi37001 Novel hum
12	1769.8	96.1	1816	12	ADL83008	Adl83008 Human PRO
13	1769.8	96.1	1816	12	ADL91876	Adl91876 Human PRO
14	1769.4	96.1	1816	3	AAZ35746	Aaz35746 Human int
15	1769.4	96.1	1816	3	AAZ52035	Aaz52035 cDNA enco
16	1769.4	96.1	1816	3	AAA75761	Aaa75761 cDNA enco
17	1607.4	87.3	2015	6	AAD28777	Aad28777 Human Int
18	1607.4	87.3	2015	6	ABA03201	Aba03201 Human IL-
19	1607.4	87.3	2015	12	ADE83328	Ade83328 Human IL-
20	1573.4	85.5	1713	6	ABA03202	Aba03202 Human IL-
21	1539	83.6	1701	3	AAA87757	Aaa87757 Human sec
22	1539	83.6	1701	5	AAF64039	Aaf64039 cDNA enco
23	1539	83.6	1701	12	ADP18777	Adp18777 Human sec
24	1513.4	82.2	1515	4	AAS46124	Aas46124 Human DNA
25	1513.4	82.2	1515	4	AAF92136	Aaf92136 Human PRO
26	1513.4	82.2	1515	4	AAS09514	Aas09514 Human cDN
27	1513.4	82.2	1515	6	ABS74456	Abs74456 Human cDN
28	1513.4	82.2	1515	8	ACA89574	Aca89574 cDNA enco
29	1513.4	82.2	1515	8	ACA73584	Aca73584 Human sec
30	1513.4	82.2	1515	8	ACA05899	Aca05899 Human sec
31	1513.4	82.2	1515	8	ACA66733	Aca66733 cDNA enco
32	1513.4	82.2	1515	8	ACA91242	Aca91242 Novel hum
33	1513.4	82.2	1515	8	ACD81619	Acd81619 Human cDN
34	1513.4	82.2	1515	8	ACF20308	Acf20308 Human sec

35	1513.4	82.2	1515	8	ACF19694	Acf19694	Human	sec
36	1513.4	82.2	1515	8	ACD21982	Acd21982	Human	sec
37	1513.4	82.2	1515	8	ACF13147	Acf13147	Human	sec
38	1513.4	82.2	1515	8	ACD25250	Acd25250	Human	sec
39	1513.4	82.2	1515	8	ACF00299	Acf00299	Human	sec
40	1513.4	82.2	1515	8	ACA60441	Aca60441	Novel	hum
41	1513.4	82.2	1515	8	ACA72356	Aca72356	Novel	hum
42	1513.4	82.2	1515	8	ACD04880	Acd04880	Novel	hum
43	1513.4	82.2	1515	8	ACD18341	Acd18341	Human	sec
44	1513.4	82.2	1515	8	ACD08348	Acd08348	Human	sec
45	1513.4	82.2	1515	8	ACA88782	Aca88782	Novel	hum

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

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SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1800.2	97.8	2171	4	US-09-976-594-762			Sequence 762, App
	2	1776.6	96.5	1918	4	US-09-268-311-17			Sequence 17, Appl
	3	1769.4	96.1	1816	4	US-09-268-311-1			Sequence 1, Appli
	4	1769.4	96.1	1816	4	US-09-154-219-1			Sequence 1, Appli
	5	1539	83.6	1701	4	US-09-599-360B-56			Sequence 56, Appl
	6	1513.4	82.2	1515	4	US-09-747-259-11			Sequence 11, Appl
	7	932.4	50.6	5105	4	US-09-919-039-293			Sequence 293, App
	8	756	41.1	2337	4	US-09-919-039-294			Sequence 294, App
	9	328	17.8	409	4	US-09-268-311-4			Sequence 4, Appli
	10	328	17.8	409	4	US-09-154-219-4			Sequence 4, Appli
	11	187.2	10.2	327	4	US-09-268-311-5			Sequence 5, Appli
	12	187.2	10.2	327	4	US-09-154-219-5			Sequence 5, Appli
	13	50	2.7	50	4	US-09-747-259-31			Sequence 31, Appl
	14	43.6	2.4	3288	2	US-08-620-694A-1			Sequence 1, Appli
	15	43.6	2.4	3288	3	US-09-022-255-1			Sequence 1, Appli
	16	43.6	2.4	3288	3	US-09-022-696-1			Sequence 1, Appli
	17	43.6	2.4	3288	3	US-08-978-773-1			Sequence 1, Appli
	18	43.6	2.4	3288	3	US-09-022-253-1			Sequence 1, Appli
	19	43.6	2.4	3288	3	US-09-022-260-1			Sequence 1, Appli
	20	43.6	2.4	3288	3	US-09-022-259-1			Sequence 1, Appli
	21	43.6	2.4	3288	3	US-09-022-257-1			Sequence 1, Appli
	22	43.6	2.4	3288	4	US-09-549-679-1			Sequence 1, Appli
	23	41.8	2.3	3719	4	US-08-956-171E-344			Sequence 344, App
	24	41.8	2.3	3719	4	US-08-781-986A-344			Sequence 344, App
c	25	41.2	2.2	2215	2	US-08-980-329C-1			Sequence 1, Appli
	26	40.4	2.2	3223	2	US-08-620-694A-9			Sequence 9, Appli
	27	40.4	2.2	3223	3	US-09-022-255-9			Sequence 9, Appli
	28	40.4	2.2	3223	3	US-09-022-696-9			Sequence 9, Appli
	29	40.4	2.2	3223	3	US-08-978-773-3			Sequence 3, Appli
	30	40.4	2.2	3223	3	US-09-022-253-9			Sequence 9, Appli
	31	40.4	2.2	3223	3	US-09-022-260-9			Sequence 9, Appli
	32	40.4	2.2	3223	3	US-09-022-259-9			Sequence 9, Appli
	33	40.4	2.2	3223	3	US-09-022-257-9			Sequence 9, Appli
	34	40.4	2.2	3223	4	US-09-549-679-9			Sequence 9, Appli
c	35	40	2.2	1350	4	US-09-248-796A-8476			Sequence 8476, Ap
c	36	40	2.2	11015	4	US-10-204-708-56			Sequence 56, Appl
	37	40	2.2	58407	4	US-08-916-421B-2			Sequence 2, Appli
	38	40	2.2	58407	4	US-09-692-570-2			Sequence 2, Appli
c	39	39.8	2.2	5433	3	US-08-929-329-1			Sequence 1, Appli
c	40	39.4	2.1	6113	4	US-10-204-708-14			Sequence 14, Appl

	41	39	2.1	640681	4	US-09-790-988-1	Sequence 1, Appli
	42	38.8	2.1	238	4	US-09-016-434-560	Sequence 560, App
	43	38.8	2.1	238	4	US-09-023-655-561	Sequence 561, App
C	44	38.8	2.1	399	4	US-09-621-976-8976	Sequence 8976, Ap
	45	38	2.1	3942	4	US-09-601-198-50	Sequence 50, Appl

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1841	100.0	1841	9	US-09-886-404-17	Sequence 17, Appl
2	1841	100.0	1841	15	US-10-037-591A-17	Sequence 17, Appl
3	1805	98.0	1818	16	US-10-169-395-56	Sequence 56, Appl
4	1790.2	97.2	1796	10	US-09-863-818A-1	Sequence 1, Appli
5	1790.2	97.2	1796	18	US-10-749-144-1	Sequence 1, Appli
6	1786	97.0	1827	9	US-09-778-971-1	Sequence 1, Appli
7	1776.6	96.5	1918	11	US-09-796-844-17	Sequence 17, Appl
8	1776.6	96.5	1918	17	US-10-645-702-17	Sequence 17, Appl
9	1769.8	96.1	1816	17	US-10-614-853-1	Sequence 1, Appli
10	1769.4	96.1	1816	11	US-09-796-844-1	Sequence 1, Appli
11	1769.4	96.1	1816	17	US-10-645-702-1	Sequence 1, Appli
12	1769.4	96.1	1816	17	US-10-686-639-1	Sequence 1, Appli
13	1607.4	87.3	2015	9	US-09-886-404-19	Sequence 19, Appl
14	1607.4	87.3	2015	15	US-10-037-591A-19	Sequence 19, Appl
15	1539	83.6	1701	11	US-09-978-360A-33	Sequence 33, Appl
16	1539	83.6	1701	15	US-10-315-664-56	Sequence 56, Appl
17	1513.4	82.2	1515	9	US-09-874-503-11	Sequence 11, Appl
18	1513.4	82.2	1515	10	US-09-747-259-11	Sequence 11, Appl
19	1513.4	82.2	1515	10	US-09-908-827-11	Sequence 11, Appl
20	1513.4	82.2	1515	13	US-10-006-867-157	Sequence 157, App
21	1513.4	82.2	1515	13	US-10-052-586-399	Sequence 399, App
22	1513.4	82.2	1515	13	US-10-063-547-157	Sequence 157, App
23	1513.4	82.2	1515	13	US-10-000-157-11	Sequence 11, Appl
24	1513.4	82.2	1515	13	US-10-063-551-157	Sequence 157, App
25	1513.4	82.2	1515	14	US-10-174-590-399	Sequence 399, App

26	1513.4	82.2	1515	14	US-10-176-758-399	Sequence 399, App
27	1513.4	82.2	1515	14	US-10-175-737-399	Sequence 399, App
28	1513.4	82.2	1515	14	US-10-063-616-157	Sequence 157, App
29	1513.4	82.2	1515	14	US-10-174-581-399	Sequence 399, App
30	1513.4	82.2	1515	14	US-10-176-483-399	Sequence 399, App
31	1513.4	82.2	1515	14	US-10-176-749-399	Sequence 399, App
32	1513.4	82.2	1515	14	US-10-176-914-399	Sequence 399, App
33	1513.4	82.2	1515	14	US-10-176-915-399	Sequence 399, App
34	1513.4	82.2	1515	14	US-10-063-569-157	Sequence 157, App
35	1513.4	82.2	1515	14	US-10-063-513-157	Sequence 157, App
36	1513.4	82.2	1515	14	US-10-063-515-157	Sequence 157, App
37	1513.4	82.2	1515	14	US-10-063-512-157	Sequence 157, App
38	1513.4	82.2	1515	14	US-10-173-706-399	Sequence 399, App
39	1513.4	82.2	1515	14	US-10-175-738-399	Sequence 399, App
40	1513.4	82.2	1515	14	US-10-175-752-399	Sequence 399, App
41	1513.4	82.2	1515	14	US-10-176-482-399	Sequence 399, App
42	1513.4	82.2	1515	14	US-10-176-757-399	Sequence 399, App
43	1513.4	82.2	1515	14	US-10-176-913-399	Sequence 399, App
44	1513.4	82.2	1515	14	US-10-180-552-399	Sequence 399, App
45	1513.4	82.2	1515	14	US-10-180-557-399	Sequence 399, App

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hlc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

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SUMMARIES

		%						
Result	Query	Match	Length	DB	ID	Description		
No.	Score							
	1	1814.2	98.5	1819	3	CR615594	CR615594 full-leng	
	2	988.4	53.7	2062	3	AK045627	AK045627 Mus muscu	
	3	974.2	52.9	2010	3	AK050139	AK050139 Mus muscu	
c	4	810.6	44.0	960	1	AL565993	AL565993 AL565993	
c	5	805.2	43.7	875	5	BX453537	BX453537 BX453537	
	6	796.2	43.2	902	1	AL535617	AL535617 AL535617	
	7	794.6	43.2	887	5	BX431018	BX431018 BX431018	
	8	766.2	41.6	946	4	BI823321	BI823321 603041231	
	9	751.8	40.8	795	7	CF455736	CF455736 AGENCOURT	
c	10	719.8	39.1	882	5	BX453536	BX453536 BX453536	
c	11	717.2	39.0	783	6	CB241389	CB241389 UI-CF-FN0	
	12	672.8	36.5	676	5	BX483104	BX483104 DKFZp686L	
	13	643.8	35.0	703	1	AV709899	AV709899 AV709899	
	14	638.4	34.7	652	4	BM693867	BM693867 UI-E-DW1-	
c	15	638.2	34.7	664	6	CB305764	CB305764 UI-CF-EN1	
	16	626.8	34.0	641	2	BE539514	BE539514 601060209	
	17	626.4	34.0	676	1	AV727345	AV727345 AV727345	
c	18	621.2	33.7	657	4	BM670929	BM670929 UI-E-DW1-	
	19	608.8	33.1	788	4	BI458542	BI458542 603198643	
c	20	603.4	32.8	630	4	BG433769	BG433769 602497744	
	21	594.6	32.3	898	5	BX431019	BX431019 BX431019	
	22	586.4	31.9	842	4	BI602183	BI602183 603244108	
	23	585.4	31.8	680	2	AW970151	AW970151 EST382232	
	24	558.4	30.3	561	2	AW675096	AW675096 bb40e05.y	
	25	524.6	28.5	745	7	CK832878	CK832878 4056654 B	
c	26	523.2	28.4	547	6	CA412162	CA412162 UI-H-EU1-	
c	27	503.2	27.3	510	2	AW299271	AW299271 xs48h02.x	
c	28	496.2	27.0	509	2	BF110326	BF110326 7n36f01.x	
c	29	481.2	26.1	488	1	AA514396	AA514396 nf57c01.s	
c	30	480.8	26.1	502	2	BE466508	BE466508 hx93h01.x	
c	31	478.4	26.0	484	2	BF064177	BF064177 7h95b11.x	
c	32	476.4	25.9	491	2	AW837146	AW837146 QV1-LT003	
	33	475.8	25.8	708	7	CK951479	CK951479 4090992 B	
	34	463.8	25.2	773	4	BI103740	BI103740 602887278	
	35	456.8	24.8	710	2	BB653710	BB653710 BB653710	
	36	452.8	24.6	468	5	BX282554	BX282554 BX282554	
c	37	441.8	24.0	457	1	AA677205	AA677205 zj60f04.s	

c	38	439.8	23.9	460	2	BF740045	BF740045	7o42g04.x
	39	437.8	23.8	470	2	BF921554	BF921554	MR1-NT017
c	40	435.4	23.7	437	1	AI032064	AI032064	ow68d12.x
c	41	434.4	23.6	477	1	AA287951	AA287951	zs55b03.r
c	42	433	23.5	435	8	AQ309936	AQ309936	CIT-HSP-2
c	43	429	23.3	499	2	BF920093	BF920093	MR1-NT017
	44	420	22.8	420	1	AV728939	AV728939	AV728939
c	45	418.4	22.7	420	1	AI401622	AI401622	tf60d02.x

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2015	100.0	2015	6	AX253207	AX253207	Sequence
2	2015	100.0	2015	6	AX365260	AX365260	Sequence
3	1607.4	79.8	1841	6	AX253204	AX253204	Sequence
4	1607.4	79.8	1841	6	AX365258	AX365258	Sequence
5	1571.4	78.0	1818	6	AX191534	AX191534	Sequence
6	1566.6	77.7	2171	6	AR448094	AR448094	Sequence
7	1561	77.5	2042	9	BC000980	BC000980	Homo sapi
8	1556.6	77.3	1796	6	AX350967	AX350967	Sequence
9	1552.4	77.0	1828	9	AF208110	AF208110	Homo sapi
10	1543	76.6	1918	6	AR256118	AR256118	Sequence
11	1536.2	76.2	1816	9	AF212365	AF212365	Homo sapi
12	1535.8	76.2	1816	6	AR256107	AR256107	Sequence
13	1535.8	76.2	1816	6	AR410121	AR410121	Sequence
14	1439	71.4	1713	6	AX253209	AX253209	Sequence
15	1432.6	71.1	1701	6	AR306577	AR306577	Sequence
16	1432.6	71.1	1701	6	AX061651	AX061651	Sequence
17	1324.6	65.7	1583	9	AF250309	AF250309	Homo sapi
18	1279.8	63.5	1515	6	AR338361	AR338361	Sequence
19	1279.8	63.5	1515	6	AX092426	AX092426	Sequence
20	1279.8	63.5	1515	6	AX180774	AX180774	Sequence
21	1279.8	63.5	1515	6	AX376332	AX376332	Sequence
22	1279.8	63.5	1515	9	AY359122	AY359122	Homo sapi
23	1272.2	63.1	1509	6	AX191524	AX191524	Sequence
24	1270.6	63.1	1509	12	BT007692	BT007692	Synthetic
25	1040.2	51.6	2856	9	AF208111	AF208111	Homo sapi
26	958.2	47.6	1362	6	CQ716823	CQ716823	Sequence
27	940.2	46.7	2080	6	BD275570	BD275570	MOLECULES
28	862.8	42.8	1506	6	AX350969	AX350969	Sequence
c 29	842.2	41.8	7164	6	BD185215	BD185215	Novel gen
30	842.2	41.8	22531	9	AY518533	AY518533	Homo sapi
c 31	842.2	41.8	149634	9	AC113172	AC113172	Homo sapi
c 32	842.2	41.8	177072	9	AC012467	AC012467	Homo sapi

	33	765.8	38.0	1963	10	AF208108	AF208108 Mus muscu
	34	758.4	37.6	2018	10	BC026546	BC026546 Mus muscu
	35	643.2	31.9	2589	10	AF208109	AF208109 Mus muscu
	36	378.2	18.8	234131	2	AC093357	AC093357 Mus muscu
c	37	359.4	17.8	234122	2	AC137172	AC137172 Rattus no
c	38	359.4	17.8	251412	2	AC136586	AC136586 Rattus no
	39	328	16.3	409	6	AR256108	AR256108 Sequence
	40	328	16.3	409	6	AR410122	AR410122 Sequence
c	41	263.6	13.1	507	11	G29993	G29993 human STS S
	42	204.2	10.1	374	6	AX098181	AX098181 Sequence
c	43	200.6	10.0	201	11	BV175040	BV175040 sqnm76293
	44	187.2	9.3	327	6	AR256109	AR256109 Sequence
	45	187.2	9.3	327	6	AR410123	AR410123 Sequence

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2015	100.0	2015	6	AAD28777	Aad28777 Human Int
2	2015	100.0	2015	6	ABA03201	Aba03201 Human IL-
3	2015	100.0	2015	12	ADE83328	Ade83328 Human IL-
4	1607.4	79.8	1841	6	AAD28776	Aad28776 Human Int
5	1607.4	79.8	1841	6	ABA03200	Aba03200 Human IL-
6	1607.4	79.8	1841	12	ADE83326	Ade83326 Human IL-
7	1571.4	78.0	1818	4	AAD12581	Aad12581 Human pro
8	1566.6	77.7	2171	12	ADL13033	Adl13033 Human ste
9	1557	77.3	2161	4	AAH99008	Aah99008 Human EST
10	1556.6	77.3	1796	6	AAS18126	Aas18126 Human DNA
11	1552.4	77.0	1827	4	AAD13443	Aad13443 Human int
12	1543	76.6	1918	3	AAZ52046	Aaz52046 cDNA enco
13	1543	76.6	1918	3	AAA75772	Aaa75772 cDNA enco
14	1536.2	76.2	1816	12	ADI37001	Adi37001 Novel hum
15	1536.2	76.2	1816	12	ADL83008	Adl83008 Human PRO
16	1536.2	76.2	1816	12	ADL91876	Adl91876 Human PRO
17	1535.8	76.2	1816	3	AAZ35746	Aaz35746 Human int
18	1535.8	76.2	1816	3	AAZ52035	Aaz52035 cDNA enco
19	1535.8	76.2	1816	3	AAA75761	Aaa75761 cDNA enco
20	1439	71.4	1713	6	ABA03202	Aba03202 Human IL-
21	1432.6	71.1	1701	3	AAA87757	Aaa87757 Human sec
22	1432.6	71.1	1701	5	AAF64039	Aaf64039 cDNA enco
23	1432.6	71.1	1701	12	ADP18777	Adp18777 Human sec
24	1279.8	63.5	1515	4	AAS46124	Aas46124 Human DNA
25	1279.8	63.5	1515	4	AAF92136	Aaf92136 Human PRO
26	1279.8	63.5	1515	4	AAS09514	Aas09514 Human cDN
27	1279.8	63.5	1515	6	ABS74456	Abs74456 Human cDN
28	1279.8	63.5	1515	8	ACA89574	Aca89574 cDNA enco
29	1279.8	63.5	1515	8	ACA73584	Aca73584 Human sec
30	1279.8	63.5	1515	8	ACA05899	Aca05899 Human sec
31	1279.8	63.5	1515	8	ACA66733	Aca66733 cDNA enco
32	1279.8	63.5	1515	8	ACA91242	Aca91242 Novel hum
33	1279.8	63.5	1515	8	ACD81619	Acd81619 Human cDN
34	1279.8	63.5	1515	8	ACF20308	Acf20308 Human sec

35	1279.8	63.5	1515	8	ACF19694	Acf19694	Human	sec
36	1279.8	63.5	1515	8	ACD21982	Acd21982	Human	sec
37	1279.8	63.5	1515	8	ACF13147	Acf13147	Human	sec
38	1279.8	63.5	1515	8	ACD25250	Acd25250	Human	sec
39	1279.8	63.5	1515	8	ACF00299	Acf00299	Human	sec
40	1279.8	63.5	1515	8	ACA60441	Aca60441	Novel	hum
41	1279.8	63.5	1515	8	ACA72356	Aca72356	Novel	hum
42	1279.8	63.5	1515	8	ACD04880	Acd04880	Novel	hum
43	1279.8	63.5	1515	8	ACD18341	Acd18341	Human	sec
44	1279.8	63.5	1515	8	ACD08348	Acd08348	Human	sec
45	1279.8	63.5	1515	8	ACA88782	Aca88782	Novel	hum

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2015	100.0	2015	9	US-09-886-404-19	Sequence 19, Appl
2	2015	100.0	2015	15	US-10-037-591A-19	Sequence 19, Appl
3	1607.4	79.8	1841	9	US-09-886-404-17	Sequence 17, Appl
4	1607.4	79.8	1841	15	US-10-037-591A-17	Sequence 17, Appl
5	1571.4	78.0	1818	16	US-10-169-395-56	Sequence 56, Appl
6	1556.6	77.3	1796	10	US-09-863-818A-1	Sequence 1, Appli
7	1556.6	77.3	1796	18	US-10-749-144-1	Sequence 1, Appli
8	1552.4	77.0	1827	9	US-09-778-971-1	Sequence 1, Appli
9	1543	76.6	1918	11	US-09-796-844-17	Sequence 17, Appl
10	1543	76.6	1918	17	US-10-645-702-17	Sequence 17, Appl
11	1536.2	76.2	1816	17	US-10-614-853-1	Sequence 1, Appli
12	1535.8	76.2	1816	11	US-09-796-844-1	Sequence 1, Appli
13	1535.8	76.2	1816	17	US-10-645-702-1	Sequence 1, Appli
14	1535.8	76.2	1816	17	US-10-686-639-1	Sequence 1, Appli
15	1432.6	71.1	1701	11	US-09-978-360A-33	Sequence 33, Appl
16	1432.6	71.1	1701	15	US-10-315-664-56	Sequence 56, Appl
17	1279.8	63.5	1515	9	US-09-874-503-11	Sequence 11, Appl
18	1279.8	63.5	1515	10	US-09-747-259-11	Sequence 11, Appl
19	1279.8	63.5	1515	10	US-09-908-827-11	Sequence 11, Appl
20	1279.8	63.5	1515	13	US-10-006-867-157	Sequence 157, App
21	1279.8	63.5	1515	13	US-10-052-586-399	Sequence 399, App
22	1279.8	63.5	1515	13	US-10-063-547-157	Sequence 157, App
23	1279.8	63.5	1515	13	US-10-000-157-11	Sequence 11, Appl
24	1279.8	63.5	1515	13	US-10-063-551-157	Sequence 157, App
25	1279.8	63.5	1515	14	US-10-174-590-399	Sequence 399, App

26	1279.8	63.5	1515	14	US-10-176-758-399	Sequence 399, App
27	1279.8	63.5	1515	14	US-10-175-737-399	Sequence 399, App
28	1279.8	63.5	1515	14	US-10-063-616-157	Sequence 157, App
29	1279.8	63.5	1515	14	US-10-174-581-399	Sequence 399, App
30	1279.8	63.5	1515	14	US-10-176-483-399	Sequence 399, App
31	1279.8	63.5	1515	14	US-10-176-749-399	Sequence 399, App
32	1279.8	63.5	1515	14	US-10-176-914-399	Sequence 399, App
33	1279.8	63.5	1515	14	US-10-176-915-399	Sequence 399, App
34	1279.8	63.5	1515	14	US-10-063-569-157	Sequence 157, App
35	1279.8	63.5	1515	14	US-10-063-513-157	Sequence 157, App
36	1279.8	63.5	1515	14	US-10-063-515-157	Sequence 157, App
37	1279.8	63.5	1515	14	US-10-063-512-157	Sequence 157, App
38	1279.8	63.5	1515	14	US-10-173-706-399	Sequence 399, App
39	1279.8	63.5	1515	14	US-10-175-738-399	Sequence 399, App
40	1279.8	63.5	1515	14	US-10-175-752-399	Sequence 399, App
41	1279.8	63.5	1515	14	US-10-176-482-399	Sequence 399, App
42	1279.8	63.5	1515	14	US-10-176-757-399	Sequence 399, App
43	1279.8	63.5	1515	14	US-10-176-913-399	Sequence 399, App
44	1279.8	63.5	1515	14	US-10-180-552-399	Sequence 399, App
45	1279.8	63.5	1515	14	US-10-180-557-399	Sequence 399, App

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	1566.6	77.7	2171	4	US-09-976-594-762	Sequence 762, App
	2	1543	76.6	1918	4	US-09-268-311-17	Sequence 17, Appl
	3	1535.8	76.2	1816	4	US-09-268-311-1	Sequence 1, Appli
	4	1535.8	76.2	1816	4	US-09-154-219-1	Sequence 1, Appli
	5	1432.6	71.1	1701	4	US-09-599-360B-56	Sequence 56, Appl
	6	1279.8	63.5	1515	4	US-09-747-259-11	Sequence 11, Appl
	7	932.4	46.3	5105	4	US-09-919-039-293	Sequence 293, App
	8	522.4	25.9	2337	4	US-09-919-039-294	Sequence 294, App
	9	328	16.3	409	4	US-09-268-311-4	Sequence 4, Appli
	10	328	16.3	409	4	US-09-154-219-4	Sequence 4, Appli
	11	187.2	9.3	327	4	US-09-268-311-5	Sequence 5, Appli
	12	187.2	9.3	327	4	US-09-154-219-5	Sequence 5, Appli
c	13	144.2	7.2	282	1	US-08-133-629-8	Sequence 8, Appli
c	14	144	7.1	272	4	US-09-513-999C-19511	Sequence 19511, A
c	15	141.8	7.0	283	4	US-08-579-445-26	Sequence 26, Appl
c	16	140.6	7.0	1154	4	US-09-539-333D-37	Sequence 37, Appl
c	17	140.6	7.0	1301	4	US-09-539-333D-36	Sequence 36, Appl
c	18	140.6	7.0	1386	4	US-09-539-333D-40	Sequence 40, Appl
c	19	140.6	7.0	319608	4	US-09-679-409-1	Sequence 1, Appli
c	20	140.2	7.0	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	21	140	6.9	6769	1	US-08-480-784-20	Sequence 20, Appl
c	22	140	6.9	6769	1	US-08-483-553-20	Sequence 20, Appl
c	23	140	6.9	6769	1	US-08-487-002-20	Sequence 20, Appl
c	24	140	6.9	6769	1	US-08-483-554B-20	Sequence 20, Appl
c	25	140	6.9	6769	1	US-08-488-011B-20	Sequence 20, Appl
c	26	140	6.9	6769	3	US-08-850-727-20	Sequence 20, Appl
c	27	140	6.9	6769	5	PCT-US95-10202-20	Sequence 20, Appl
c	28	140	6.9	6769	5	PCT-US95-10203-20	Sequence 20, Appl
c	29	140	6.9	6769	5	PCT-US95-10220-20	Sequence 20, Appl
	30	138.8	6.9	45546	3	US-09-146-053-6	Sequence 6, Appli
c	31	137	6.8	55827	4	US-09-813-133A-3	Sequence 3, Appli
	32	137	6.8	87350	3	US-08-781-891-79	Sequence 79, Appl
	33	137	6.8	87350	4	US-09-618-166-79	Sequence 79, Appl
	34	137	6.8	87543	4	US-09-791-211-3	Sequence 3, Appli
	35	137	6.8	174493	4	US-09-804-471A-3	Sequence 3, Appli
	36	137	6.8	174493	4	US-10-238-709-3	Sequence 3, Appli
	37	136.8	6.8	4171	4	US-09-667-422-3	Sequence 3, Appli
c	38	136.8	6.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
c	39	136.8	6.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
c	40	136.8	6.8	246240	2	US-08-724-394A-22	Sequence 22, Appl

	41	136.4	6.8	511	4	US-09-621-976-1354	Sequence 1354, Ap
C	42	136.4	6.8	3663	3	US-09-499-884-11	Sequence 11, Appl
	43	136.4	6.8	114793	4	US-10-148-806-3	Sequence 3, Appli
C	44	136	6.7	9278	1	US-08-243-542-9	Sequence 9, Appli
C	45	136	6.7	9278	1	US-08-477-407-9	Sequence 9, Appli

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_hlc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	1580.6	78.4	1819	3	CR615594	CR615594 full-leng
	2	810.6	40.2	960	1	AL565993	AL565993 AL565993
	3	794.6	39.4	887	5	BX431018	BX431018 BX431018
	4	770.6	38.2	2010	3	AK050139	AK050139 Mus muscu
	5	766	38.0	2062	3	AK045627	AK045627 Mus muscu
c	6	751.8	37.3	795	7	CF455736	CF455736 AGENCOURT
	7	717.2	35.6	783	6	CB241389	CB241389 UI-CF-FN0
	8	639.8	31.8	875	5	BX453537	BX453537 BX453537
	9	638.4	31.7	652	4	BM693867	BM693867 UI-E-DW1-
	10	638.2	31.7	664	6	CB305764	CB305764 UI-CF-EN1
c	11	626.8	31.1	641	2	BE539514	BE539514 601060209
	12	626.4	31.1	676	1	AV727345	AV727345 AV727345
	13	621.2	30.8	657	4	BM670929	BM670929 UI-E-DW1-
	14	614.8	30.5	882	5	BX453536	BX453536 BX453536
	15	611.8	30.4	788	4	BI458542	BI458542 603198643
c	16	607.4	30.1	902	1	AL535617	AL535617 AL535617
	17	603.4	29.9	630	4	BG433769	BG433769 602497744
	18	594.6	29.5	898	5	BX431019	BX431019 BX431019
	19	589.4	29.3	842	4	BI602183	BI602183 603244108
	20	585.4	29.1	680	2	AW970151	AW970151 EST382232
c	21	564.2	28.0	703	1	AV709899	AV709899 AV709899
	22	532.6	26.4	946	4	BI823321	BI823321 603041231
	23	523.2	26.0	547	6	CA412162	CA412162 UI-H-EU1-
	24	503.2	25.0	510	2	AW299271	AW299271 xs48h02.x
	25	496.2	24.6	509	2	BF110326	BF110326 7n36f01.x
c	26	481.2	23.9	488	1	AA514396	AA514396 nf57c01.s
	27	480.8	23.9	502	2	BE466508	BE466508 hx93h01.x
	28	478.4	23.7	484	2	BF064177	BF064177 7h95b11.x
	29	476.4	23.6	491	2	AW837146	AW837146 QV1-LT003
	30	474.8	23.6	708	7	CK951479	CK951479 4090992 B
c	31	452.8	22.5	468	5	BX282554	BX282554 BX282554
	32	441.8	21.9	457	1	AA677205	AA677205 zj60f04.s
	33	439.8	21.8	460	2	BF740045	BF740045 7o42g04.x
	34	439.2	21.8	676	5	BX483104	BX483104 DKFZp686L
	35	437.8	21.7	470	2	BF921554	BF921554 MR1-NT017
c	36	435.4	21.6	437	1	AI032064	AI032064 ow68d12.x
	37	434.4	21.6	477	1	AA287951	AA287951 zs55b03.r

C	38	433	21.5	435	8	AQ309936	AQ309936	CIT-HSP-2
C	39	429	21.3	499	2	BF920093	BF920093	MR1-NT017
	40	420	20.8	420	1	AV728939	AV728939	AV728939
C	41	418.4	20.8	420	1	AI401622	AI401622	tf60d02.x
	42	417.4	20.7	419	1	AV728945	AV728945	AV728945
C	43	416.6	20.7	434	1	AI826949	AI826949	wk57b12.x
C	44	412.2	20.5	427	1	AI627783	AI627783	ty82a11.x
C	45	410	20.3	414	1	AI911549	AI911549	ty73d09.x

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	1713	100.0	1713	6	AX253209	AX253209 Sequence	
2	1678.6	98.0	1701	6	AR306577	AR306577 Sequence	
3	1678.6	98.0	1701	6	AX061651	AX061651 Sequence	
4	1573.4	91.9	1841	6	AX253204	AX253204 Sequence	
5	1573.4	91.9	1841	6	AX365258	AX365258 Sequence	
6	1540.6	89.9	1818	6	AX191534	AX191534 Sequence	
7	1532.6	89.5	2171	6	AR448094	AR448094 Sequence	
8	1530.2	89.3	2042	9	BC000980	BC000980 Homo sapi	
9	1525.8	89.1	1796	6	AX350967	AX350967 Sequence	
10	1518.4	88.6	1828	9	AF208110	AF208110 Homo sapi	
11	1509	88.1	1918	6	AR256118	AR256118 Sequence	
12	1502.2	87.7	1816	9	AF212365	AF212365 Homo sapi	
13	1501.8	87.7	1816	6	AR256107	AR256107 Sequence	
14	1501.8	87.7	1816	6	AR410121	AR410121 Sequence	
15	1439	84.0	2015	6	AX253207	AX253207 Sequence	
16	1439	84.0	2015	6	AX365260	AX365260 Sequence	
17	1293.8	75.5	1583	9	AF250309	AF250309 Homo sapi	
18	1245.8	72.7	1515	6	AR338361	AR338361 Sequence	
19	1245.8	72.7	1515	6	AX092426	AX092426 Sequence	
20	1245.8	72.7	1515	6	AX180774	AX180774 Sequence	
21	1245.8	72.7	1515	6	AX376332	AX376332 Sequence	
22	1245.8	72.7	1515	9	AY359122	AY359122 Homo sapi	
23	1241.4	72.5	1509	6	AX191524	AX191524 Sequence	
24	1239.8	72.4	1509	12	BT007692	BT007692 Synthetic	
25	1040.2	60.7	2856	9	AF208111	AF208111 Homo sapi	
26	940.2	54.9	2080	6	BD275570	BD275570 MOLECULES	
27	927.4	54.1	1362	6	CQ716823	CQ716823 Sequence	
28	855.2	49.9	1506	6	AX350969	AX350969 Sequence	
c 29	842.2	49.2	7164	6	BD185215	BD185215 Novel gen	
30	842.2	49.2	22531	9	AY518533	AY518533 Homo sapi	
c 31	842.2	49.2	149634	9	AC113172	AC113172 Homo sapi	
c 32	842.2	49.2	177072	9	AC012467	AC012467 Homo sapi	

	33	751	43.8	1963	10	AF208108	AF208108 Mus muscu
	34	743.6	43.4	2018	10	BC026546	BC026546 Mus muscu
	35	643.2	37.5	2589	10	AF208109	AF208109 Mus muscu
	36	378.2	22.1	234131	2	AC093357	AC093357 Mus muscu
c	37	359.4	21.0	234122	2	AC137172	AC137172 Rattus no
c	38	359.4	21.0	251412	2	AC136586	AC136586 Rattus no
	39	328	19.1	409	6	AR256108	AR256108 Sequence
	40	328	19.1	409	6	AR410122	AR410122 Sequence
c	41	263.6	15.4	507	11	G29993	G29993 human STS S
c	42	200.6	11.7	201	11	BV175040	BV175040 sqnm76293
	43	170.6	10.0	327	6	AR256109	AR256109 Sequence
	44	170.6	10.0	327	6	AR410123	AR410123 Sequence
	45	159	9.3	374	6	AX098181	AX098181 Sequence

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1713	100.0	1713	6	ABA03202	Aba03202 Human IL-
2	1678.6	98.0	1701	3	AAA87757	Aaa87757 Human sec
3	1678.6	98.0	1701	5	AAF64039	Aaf64039 cDNA enco
4	1678.6	98.0	1701	12	ADP18777	Adp18777 Human sec
5	1573.4	91.9	1841	6	AAD28776	Aad28776 Human Int
6	1573.4	91.9	1841	6	ABA03200	Aba03200 Human IL-
7	1573.4	91.9	1841	12	ADE83326	Ade83326 Human IL-
8	1540.6	89.9	1818	4	AAD12581	Aad12581 Human pro
9	1532.6	89.5	2171	12	ADL13033	Adl13033 Human ste
10	1526.2	89.1	2161	4	AAH99008	Aah99008 Human EST
11	1525.8	89.1	1796	6	AAS18126	Aas18126 Human DNA
12	1518.4	88.6	1827	4	AAD13443	Aad13443 Human int
13	1509	88.1	1918	3	Aaz52046	Aaz52046 cDNA enco
14	1509	88.1	1918	3	AAA75772	Aaa75772 cDNA enco
15	1502.2	87.7	1816	12	ADI37001	Adi37001 Novel hum
16	1502.2	87.7	1816	12	ADL83008	Adl83008 Human PRO
17	1502.2	87.7	1816	12	ADL91876	Adl91876 Human PRO
18	1501.8	87.7	1816	3	AAZ35746	Aaz35746 Human int
19	1501.8	87.7	1816	3	AAZ52035	Aaz52035 cDNA enco
20	1501.8	87.7	1816	3	AAA75761	Aaa75761 cDNA enco
21	1439	84.0	2015	6	AAD28777	Aad28777 Human Int
22	1439	84.0	2015	6	ABA03201	Aba03201 Human IL-
23	1439	84.0	2015	12	ADE83328	Ade83328 Human IL-
24	1397.4	81.6	1399	12	ADL22929	Adl22929 Human LP3
25	1245.8	72.7	1515	4	AAS46124	Aas46124 Human DNA
26	1245.8	72.7	1515	4	AAF92136	Aaf92136 Human PRO
27	1245.8	72.7	1515	4	AAS09514	Aas09514 Human cDN
28	1245.8	72.7	1515	6	ABS74456	Abs74456 Human cDN
29	1245.8	72.7	1515	8	ACA89574	Aca89574 cDNA enco
30	1245.8	72.7	1515	8	ACA73584	Aca73584 Human sec
31	1245.8	72.7	1515	8	ACA05899	Aca05899 Human sec
32	1245.8	72.7	1515	8	ACA66733	Aca66733 cDNA enco
33	1245.8	72.7	1515	8	ACA91242	Aca91242 Novel hum
34	1245.8	72.7	1515	8	ACD81619	Acd81619 Human cDN

35	1245.8	72.7	1515	8	ACF20308	Acf20308	Human	sec
36	1245.8	72.7	1515	8	ACF19694	Acf19694	Human	sec
37	1245.8	72.7	1515	8	ACD21982	Acd21982	Human	sec
38	1245.8	72.7	1515	8	ACF13147	Acf13147	Human	sec
39	1245.8	72.7	1515	8	ACD25250	Acd25250	Human	sec
40	1245.8	72.7	1515	8	ACF00299	Acf00299	Human	sec
41	1245.8	72.7	1515	8	ACA60441	Aca60441	Novel	hum
42	1245.8	72.7	1515	8	ACA72356	Aca72356	Novel	hum
43	1245.8	72.7	1515	8	ACD04880	Acd04880	Novel	hum
44	1245.8	72.7	1515	8	ACD18341	Acd18341	Human	sec
45	1245.8	72.7	1515	8	ACD08348	Acd08348	Human	sec

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1678.6	98.0	1701	4	US-09-599-360B-56	Sequence 56, Appl
2	1532.6	89.5	2171	4	US-09-976-594-762	Sequence 762, App
3	1509	88.1	1918	4	US-09-268-311-17	Sequence 17, Appl
4	1501.8	87.7	1816	4	US-09-268-311-1	Sequence 1, Appli
5	1501.8	87.7	1816	4	US-09-154-219-1	Sequence 1, Appli
6	1245.8	72.7	1515	4	US-09-747-259-11	Sequence 11, Appl
7	932.4	54.4	5105	4	US-09-919-039-293	Sequence 293, App
8	491.6	28.7	2337	4	US-09-919-039-294	Sequence 294, App
9	328	19.1	409	4	US-09-268-311-4	Sequence 4, Appli
10	328	19.1	409	4	US-09-154-219-4	Sequence 4, Appli
11	170.6	10.0	327	4	US-09-268-311-5	Sequence 5, Appli
12	170.6	10.0	327	4	US-09-154-219-5	Sequence 5, Appli
13	50	2.9	50	4	US-09-747-259-31	Sequence 31, Appl
14	45.6	2.7	3288	2	US-08-620-694A-1	Sequence 1, Appli
15	45.6	2.7	3288	3	US-09-022-255-1	Sequence 1, Appli
16	45.6	2.7	3288	3	US-09-022-696-1	Sequence 1, Appli
17	45.6	2.7	3288	3	US-08-978-773-1	Sequence 1, Appli
18	45.6	2.7	3288	3	US-09-022-253-1	Sequence 1, Appli
19	45.6	2.7	3288	3	US-09-022-260-1	Sequence 1, Appli
20	45.6	2.7	3288	3	US-09-022-259-1	Sequence 1, Appli
21	45.6	2.7	3288	3	US-09-022-257-1	Sequence 1, Appli
22	45.6	2.7	3288	4	US-09-549-679-1	Sequence 1, Appli
23	41.8	2.4	3719	4	US-08-956-171E-344	Sequence 344, App
24	41.8	2.4	3719	4	US-08-781-986A-344	Sequence 344, App
25	41.4	2.4	3223	2	US-08-620-694A-9	Sequence 9, Appli
26	41.4	2.4	3223	3	US-09-022-255-9	Sequence 9, Appli
27	41.4	2.4	3223	3	US-09-022-696-9	Sequence 9, Appli
28	41.4	2.4	3223	3	US-08-978-773-3	Sequence 3, Appli
29	41.4	2.4	3223	3	US-09-022-253-9	Sequence 9, Appli
30	41.4	2.4	3223	3	US-09-022-260-9	Sequence 9, Appli
31	41.4	2.4	3223	3	US-09-022-259-9	Sequence 9, Appli
32	41.4	2.4	3223	3	US-09-022-257-9	Sequence 9, Appli
33	41.4	2.4	3223	4	US-09-549-679-9	Sequence 9, Appli
c 34	41.2	2.4	2215	2	US-08-980-329C-1	Sequence 1, Appli
c 35	40	2.3	1350	4	US-09-248-796A-8476	Sequence 8476, Ap
c 36	40	2.3	11015	4	US-10-204-708-56	Sequence 56, Appl
37	40	2.3	58407	4	US-08-916-421B-2	Sequence 2, Appli
38	40	2.3	58407	4	US-09-692-570-2	Sequence 2, Appli
39	39.8	2.3	238	4	US-09-016-434-560	Sequence 560, App
40	39.8	2.3	238	4	US-09-023-655-561	Sequence 561, App

C	41	39.8	2.3	5433	3	US-08-929-329-1	Sequence 1, Appli
C	42	39.4	2.3	6113	4	US-10-204-708-14	Sequence 14, Appl
	43	39	2.3	640681	4	US-09-790-988-1	Sequence 1, Appli
C	44	38.8	2.3	399	4	US-09-621-976-8976	Sequence 8976, Ap
C	45	38.4	2.2	1141	4	US-09-806-708B-22	Sequence 22, Appl

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1678.6	98.0	1701	11	US-09-978-360A-33	Sequence 33, Appl
2	1678.6	98.0	1701	15	US-10-315-664-56	Sequence 56, Appl
3	1573.4	91.9	1841	9	US-09-886-404-17	Sequence 17, Appl
4	1573.4	91.9	1841	15	US-10-037-591A-17	Sequence 17, Appl
5	1540.6	89.9	1818	16	US-10-169-395-56	Sequence 56, Appl
6	1525.8	89.1	1796	10	US-09-863-818A-1	Sequence 1, Appli
7	1525.8	89.1	1796	18	US-10-749-144-1	Sequence 1, Appli
8	1518.4	88.6	1827	9	US-09-778-971-1	Sequence 1, Appli
9	1509	88.1	1918	11	US-09-796-844-17	Sequence 17, Appl
10	1509	88.1	1918	17	US-10-645-702-17	Sequence 17, Appl
11	1502.2	87.7	1816	17	US-10-614-853-1	Sequence 1, Appli
12	1501.8	87.7	1816	11	US-09-796-844-1	Sequence 1, Appli
13	1501.8	87.7	1816	17	US-10-645-702-1	Sequence 1, Appli
14	1501.8	87.7	1816	17	US-10-686-639-1	Sequence 1, Appli
15	1439	84.0	2015	9	US-09-886-404-19	Sequence 19, Appl
16	1439	84.0	2015	15	US-10-037-591A-19	Sequence 19, Appl
17	1245.8	72.7	1515	9	US-09-874-503-11	Sequence 11, Appl
18	1245.8	72.7	1515	10	US-09-747-259-11	Sequence 11, Appl
19	1245.8	72.7	1515	10	US-09-908-827-11	Sequence 11, Appl
20	1245.8	72.7	1515	13	US-10-006-867-157	Sequence 157, App
21	1245.8	72.7	1515	13	US-10-052-586-399	Sequence 399, App
22	1245.8	72.7	1515	13	US-10-063-547-157	Sequence 157, App
23	1245.8	72.7	1515	13	US-10-000-157-11	Sequence 11, Appl
24	1245.8	72.7	1515	13	US-10-063-551-157	Sequence 157, App
25	1245.8	72.7	1515	14	US-10-174-590-399	Sequence 399, App

26	1245.8	72.7	1515	14	US-10-176-758-399	Sequence 399, App
27	1245.8	72.7	1515	14	US-10-175-737-399	Sequence 399, App
28	1245.8	72.7	1515	14	US-10-063-616-157	Sequence 157, App
29	1245.8	72.7	1515	14	US-10-174-581-399	Sequence 399, App
30	1245.8	72.7	1515	14	US-10-176-483-399	Sequence 399, App
31	1245.8	72.7	1515	14	US-10-176-749-399	Sequence 399, App
32	1245.8	72.7	1515	14	US-10-176-914-399	Sequence 399, App
33	1245.8	72.7	1515	14	US-10-176-915-399	Sequence 399, App
34	1245.8	72.7	1515	14	US-10-063-569-157	Sequence 157, App
35	1245.8	72.7	1515	14	US-10-063-513-157	Sequence 157, App
36	1245.8	72.7	1515	14	US-10-063-515-157	Sequence 157, App
37	1245.8	72.7	1515	14	US-10-063-512-157	Sequence 157, App
38	1245.8	72.7	1515	14	US-10-173-706-399	Sequence 399, App
39	1245.8	72.7	1515	14	US-10-175-738-399	Sequence 399, App
40	1245.8	72.7	1515	14	US-10-175-752-399	Sequence 399, App
41	1245.8	72.7	1515	14	US-10-176-482-399	Sequence 399, App
42	1245.8	72.7	1515	14	US-10-176-757-399	Sequence 399, App
43	1245.8	72.7	1515	14	US-10-176-913-399	Sequence 399, App
44	1245.8	72.7	1515	14	US-10-180-552-399	Sequence 399, App
45	1245.8	72.7	1515	14	US-10-180-557-399	Sequence 399, App

Title: US-09-810-927B-6
 Perfect score: 1713
 Sequence: 1 ataaaagcgcagcgtgcggg.....aacaataaagcatcttcagc 1713

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	1546.6	90.3	1819	3	CR615594	CR615594 full-leng
	2	810.6	47.3	960	1	AL565993	AL565993 AL565993
	3	794.6	46.4	887	5	BX431018	BX431018 BX431018
	4	751.8	43.9	795	7	CF455736	CF455736 AGENCOURT
	5	751.2	43.9	2062	3	AK045627	AK045627 Mus muscu
c	6	747	43.6	2010	3	AK050139	AK050139 Mus muscu
	7	717.2	41.9	783	6	CB241389	CB241389 UI-CF-FN0
	8	641.2	37.4	875	5	BX453537	BX453537 BX453537
	9	638.4	37.3	652	4	BM693867	BM693867 UI-E-DW1-
	10	638.2	37.3	664	6	CB305764	CB305764 UI-CF-EN1
c	11	626.8	36.6	641	2	BE539514	BE539514 601060209
	12	626.4	36.6	676	1	AV727345	AV727345 AV727345
	13	621.2	36.3	657	4	BM670929	BM670929 UI-E-DW1-
	14	616.2	36.0	882	5	BX453536	BX453536 BX453536
	15	611	35.7	788	4	BI458542	BI458542 603198643
c	16	603.4	35.2	630	4	BG433769	BG433769 602497744
	17	594.6	34.7	898	5	BX431019	BX431019 BX431019
	18	588.6	34.4	842	4	BI602183	BI602183 603244108
	19	585.4	34.2	680	2	AW970151	AW970151 EST382232

	20	568.2	33.2	902	1	AL535617	AL535617	AL535617
	21	565.6	33.0	703	1	AV709899	AV709899	AV709899
c	22	523.2	30.5	547	6	CA412162	CA412162	UI-H-EU1-
c	23	503.2	29.4	510	2	AW299271	AW299271	xs48h02.x
	24	501.8	29.3	946	4	BI823321	BI823321	603041231
c	25	496.2	29.0	509	2	BF110326	BF110326	7n36f01.x
c	26	481.2	28.1	488	1	AA514396	AA514396	nf57c01.s
c	27	480.8	28.1	502	2	BE466508	BE466508	hx93h01.x
c	28	478.4	27.9	484	2	BF064177	BF064177	7h95b11.x
c	29	476.4	27.8	491	2	AW837146	AW837146	QV1-LT003
	30	474.8	27.7	708	7	CK951479	CK951479	4090992 B
	31	452.8	26.4	468	5	BX282554	BX282554	BX282554
c	32	441.8	25.8	457	1	AA677205	AA677205	zj60f04.s
c	33	439.8	25.7	460	2	BF740045	BF740045	7o42g04.x
	34	437.8	25.6	470	2	BF921554	BF921554	MR1-NT017
c	35	435.4	25.4	437	1	AI032064	AI032064	ow68d12.x
c	36	434.4	25.4	477	1	AA287951	AA287951	zs55b03.r
c	37	433	25.3	435	8	AQ309936	AQ309936	CIT-HSP-2
c	38	429	25.0	499	2	BF920093	BF920093	MR1-NT017
	39	420	24.5	420	1	AV728939	AV728939	AV728939
c	40	418.4	24.4	420	1	AI401622	AI401622	tf60d02.x
	41	417.4	24.4	419	1	AV728945	AV728945	AV728945
c	42	416.6	24.3	434	1	AI826949	AI826949	wk57b12.x
c	43	412.2	24.1	427	1	AI627783	AI627783	ty82a11.x
c	44	410	23.9	414	1	AI911549	AI911549	ty73d09.x
c	45	407.2	23.8	416	2	BE047352	BE047352	hq79e01.x